

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/690,246A

Source: 1/FW16

Date Processed by STIC: 8/8/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 08/08/2005

PATENT APPLICATION: US/10/690,246A

TIME: 10:07:30

Input Set : A:\U0148638 sequence.txt

Output Set: N:\CRF4\08082005\J690246A.raw

3 <110> APPLICANT: CHEN, HONG-HWA
 4 TSAI, WEN-CHIEH
 5 CHEN, WEN-HUEI
 7 <120> TITLE OF INVENTION: DNA MOLECULE ENCODING DEF-LIKE MADS-BOX-GENES FROM
 PHALAEOPSIS
 8 ORCHID
 10 <130> FILE REFERENCE: U 014863-8
 12 <140> CURRENT APPLICATION NUMBER: 10/690,246A
 13 <141> CURRENT FILING DATE: 2003-10-21
 15 <150> PRIOR APPLICATION NUMBER: TW 091125320
 16 <151> PRIOR FILING DATE: 2002-10-25
 18 <160> NUMBER OF SEQ ID NOS: 48
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 917
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Phalaenopsis equestris
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (76)..(759)
 32 <400> SEQUENCE: 1

P.6

33	acgcgggata gtagaggaag aagaagagaa ggggttgagaa cagaggaaaa caggggagaa	60
35	caggggaaga gagag atg ggg agg ggg aag ata gag ata aaa aag ata gag	111
36	Met Gly Arg Gly Lys Ile Glu Ile Lys Lys Ile Glu	
37	1 5 10	
39	aat ccg acg aac agg caa gtt aca tat tct aag agg aga gtt ggg ata	159
40	Asn Pro Thr Asn Arg Gln Val Thr Tyr Ser Lys Arg Arg Val Gly Ile	
41	15 20 25	
43	ctg aag aag gcc aag gag ctc act gtt ctc tgt gat gct cag gtc tct	207
44	Leu Lys Lys Ala Lys Glu Leu Thr Val Leu Cys Asp Ala Gln Val Ser	
45	30 35 40	
47	ctc atc atg ttc tca agc aca gga aag ttg gct gat tac tgc agc ccc	255
48	Leu Ile Met Phe Ser Ser Thr Gly Lys Leu Ala Asp Tyr Cys Ser Pro	
49	45 50 55 60	
51	tct act gat att aag ggg ata tat gag agg tac cag gtt gtg act gga	303
52	Ser Thr Asp Ile Lys Gly Ile Tyr Glu Arg Tyr Gln Val Val Thr Gly	
53	65 70 75	
55	atg gat cta tgg aat gct cag tat gag agg atg cag aat acg ctg aag	351
56	Met Asp Leu Trp Asn Ala Gln Tyr Glu Arg Met Gln Asn Thr Leu Lys	
57	80 85 90	
59	cat ctg aat gag att aac caa aac ctg agg aag gag att agg agg agg	399
60	His Leu Asn Glu Ile Asn Gln Asn Leu Arg Lys Glu Ile Arg Arg Arg	
61	95 100 105	
63	aag ggg gag gaa ttg gag ggc atg gac ata aag caa ctg cgc ggt ctt	447

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64 Lys Gly Glu Glu Leu Glu Gly Met Asp Ile Lys Gln Leu Arg Gly Leu
65      110                      115                      120
67 gag caa act ttg gaa gag tct ctt aga att gtt agg cat aga aag tat      495
68 Glu Gln Thr Leu Glu Glu Ser Leu Arg Ile Val Arg His Arg Lys Tyr
69 125                      130                      135                      140
71 cat gtg atc gcc aca caa act gac act tac aag aaa aag ctt aaa agc      543
72 His Val Ile Ala Thr Gln Thr Asp Thr Tyr Lys Lys Lys Leu Lys Ser
73                      145                      150                      155
75 aca agg gaa act tac cgc gct cta ata cat gaa ctg gat atg aaa gag      591
76 Thr Arg Glu Thr Tyr Arg Ala Leu Ile His Glu Leu Asp Met Lys Glu
77                      160                      165                      170
79 gag aat ccg aac tac ggt ttt aat gta gaa aac cag agt aga att tat      639
80 Glu Asn Pro Asn Tyr Gly Phe Asn Val Glu Asn Gln Ser Arg Ile Tyr
81      175                      180                      185
83 gaa aat tcg att cca atg gtg aat gag tgt cct cag atg ttt tcc ttt      687
84 Glu Asn Ser Ile Pro Met Val Asn Glu Cys Pro Gln Met Phe Ser Phe
85      190                      195                      200
87 agg gtt gtt cat ccg aat cag ccc aat ctg ctt ggt tta ggt tat gaa      735
88 Arg Val Val His Pro Asn Gln Pro Asn Leu Leu Gly Leu Gly Tyr Glu
89 205                      210                      215                      220
91 tca cat gat ctt agc ctt gca taa tgagcagtaa tattatgatt ttattgtatt      789
92 Ser His Asp Leu Ser Leu Ala
93                      225
95 tttatttttat gtttgaaact ttagaattat gagatggggg atctattcag agagaactgt      849
97 cctttaattt gattttcccg tttgtttcct cttcatgtcc agtgaaattt tttgttttgt      909
99 tttttcgg      917
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 227
104 <212> TYPE: PRT
105 <213> ORGANISM: Phalaenopsis equestris
107 <400> SEQUENCE: 2
109 Met Gly Arg Gly Lys Ile Glu Ile Lys Lys Ile Glu Asn Pro Thr Asn
110 1      5      10      15
113 Arg Gln Val Thr Tyr Ser Lys Arg Arg Val Gly Ile Leu Lys Lys Ala
114      20      25      30
117 Lys Glu Leu Thr Val Leu Cys Asp Ala Gln Val Ser Leu Ile Met Phe
118      35      40      45
121 Ser Ser Thr Gly Lys Leu Ala Asp Tyr Cys Ser Pro Ser Thr Asp Ile
122      50      55      60
125 Lys Gly Ile Tyr Glu Arg Tyr Gln Val Val Thr Gly Met Asp Leu Trp
126 65      70      75      80
129 Asn Ala Gln Tyr Glu Arg Met Gln Asn Thr Leu Lys His Leu Asn Glu
130      85      90      95
133 Ile Asn Gln Asn Leu Arg Lys Glu Ile Arg Arg Arg Lys Gly Glu Glu
134      100      105      110
137 Leu Glu Gly Met Asp Ile Lys Gln Leu Arg Gly Leu Glu Gln Thr Leu
138      115      120      125
141 Glu Glu Ser Leu Arg Ile Val Arg His Arg Lys Tyr His Val Ile Ala
142      130      135      140

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145 Thr Gln Thr Asp Thr Tyr Lys Lys Lys Leu Lys Ser Thr Arg Glu Thr
146 145                               150                               155                               160
149 Tyr Arg Ala Leu Ile His Glu Leu Asp Met Lys Glu Glu Asn Pro Asn
150                               165                               170                               175
153 Tyr Gly Phe Asn Val Glu Asn Gln Ser Arg Ile Tyr Glu Asn Ser Ile
154                               180                               185                               190
157 Pro Met Val Asn Glu Cys Pro Gln Met Phe Ser Phe Arg Val Val His
158                               195                               200                               205
161 Pro Asn Gln Pro Asn Leu Leu Gly Leu Gly Tyr Glu Ser His Asp Leu
162 210                               215                               220
165 Ser Leu Ala
166 225
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 980
171 <212> TYPE: DNA
172 <213> ORGANISM: Phalaenopsis equestris
175 <220> FEATURE:
176 <221> NAME/KEY: CDS
177 <222> LOCATION: (196)..(864)
179 <400> SEQUENCE: 3
180 acgccacaac ccttttgcca ttgcctgcta atggaaaccc agctgccact ttttccttcc 60
182 ccagccttat ataccttcag ttactctctt ctgcctccat tttataaagc atactttrcc 120
184 ccttttcttt cccatatcaa tctcaactcc ttcgcttctc ctgctgcttt gggaagcaga 180
186 gcaagaaaga gaacc atg ggg agg ggg aag atc gag ata aag aag att gag 231
187 Met Gly Arg Gly Lys Ile Glu Ile Lys Lys Ile Glu
188 1 5 10
190 aac cct aca aac agg cag gtt act tac tct aag agg agg gct ggg atc 279
191 Asn Pro Thr Asn Arg Gln Val Thr Tyr Ser Lys Arg Arg Ala Gly Ile
192 15 20 25
194 atg aaa aag gcg agc gag ctc acg gtt ctc tgt gat gct cag ctc tcc 327
195 Met Lys Lys Ala Ser Glu Leu Thr Val Leu Cys Asp Ala Gln Leu Ser
196 30 35 40
198 ctt gtt atg ttc tcc agc acc ggc aag ttc tcc gag tat tgt agt cct 375
199 Leu Val Met Phe Ser Ser Thr Gly Lys Phe Ser Glu Tyr Cys Ser Pro
200 45 50 55 60
202 acc acc gat acc aag agt gta tat gat cgt tac cag cag gtg tcc ggc 423
203 Thr Thr Asp Thr Lys Ser Val Tyr Asp Arg Tyr Gln Gln Val Ser Gly
204 65 70 75
206 ata aat tta tgg agc gag cag tac gag aag atg cag aat acg ttg aat 471
207 Ile Asn Leu Trp Ser Glu Gln Tyr Glu Lys Met Gln Asn Thr Leu Asn
208 80 85 90
210 cat ttg aag gag ata aac cac aac ttg agg agg gag ata agg cag agg 519
211 His Leu Lys Glu Ile Asn His Asn Leu Arg Arg Glu Ile Arg Gln Arg
212 95 100 105
214 atg ggc gag gat ctt gaa ggg cta gaa atc aaa gaa ctg cgt ggt ctt 567
215 Met Gly Glu Asp Leu Glu Leu Glu Ile Lys Glu Leu Arg Gly Leu
216 110 115 120
218 gag caa aat atg gac gag gcc cta aag ctt gta agg aat cga aag tat 615
219 Glu Gln Asn Met Asp Glu Ala Leu Lys Leu Val Arg Asn Arg Lys Tyr

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220 125          130          135          140
222 cac gtc atc agc acc cag aca gat aca ttc aaa aaa aag ttg aaa aac      663
223 His Val Ile Ser Thr Gln Thr Asp Thr Phe Lys Lys Lys Leu Lys Asn
224          145          150          155
226 tct caa gaa acc cac agg aac tta ctc cgg gag ctg gaa act gag cac      711
227 Ser Gln Glu Thr His Arg Asn Leu Leu Arg Glu Leu Glu Thr Glu His
228          160          165          170
230 gcc gtc tac tac gtg gat gat gat cca aac aac tat gat ggc gcg ctt      759
231 Ala Val Tyr Tyr Val Asp Asp Asp Pro Asn Asn Tyr Asp Gly Ala Leu
232          175          180          185
234 gca ctt gga aat ggg gct tcc tac ttg tat tca ttt cgt acc caa cca      807
235 Ala Leu Gly Asn Gly Ala Ser Tyr Leu Tyr Ser Phe Arg Thr Gln Pro
236          190          195          200
238 agc cag ccg aac ctt cag gga gtt gga tat gtc cct cat gat cta cgt      855
239 Ser Gln Pro Asn Leu Gln Gly Val Gly Tyr Val Pro His Asp Leu Arg
240 205          210          215          220
242 ctc gcc tga tcttttatta tctgcatgcc aactgcttaa ttatatctat      904
243 Leu Ala
246 gtatctgatg ttcttacgct tacaagtagg gtctagcact gcaatcgaat tcccgcggcc      964
248 gccagcggcc ggactc      980
251 <210> SEQ ID NO: 4
252 <211> LENGTH: 222
253 <212> TYPE: PRT
254 <213> ORGANISM: Phalaenopsis equestris
256 <400> SEQUENCE: 4
258 Met Gly Arg Gly Lys Ile Glu Ile Lys Lys Ile Glu Asn Pro Thr Asn
259 1          5          10          15
262 Arg Gln Val Thr Tyr Ser Lys Arg Arg Ala Gly Ile Met Lys Lys Ala
263          20          25          30
266 Ser Glu Leu Thr Val Leu Cys Asp Ala Gln Leu Ser Leu Val Met Phe
267          35          40          45
270 Ser Ser Thr Gly Lys Phe Ser Glu Tyr Cys Ser Pro Thr Thr Asp Thr
271          50          55          60
274 Lys Ser Val Tyr Asp Arg Tyr Gln Gln Val Ser Gly Ile Asn Leu Trp
275 65          70          75          80
278 Ser Glu Gln Tyr Glu Lys Met Gln Asn Thr Leu Asn His Leu Lys Glu
279          85          90          95
282 Ile Asn His Asn Leu Arg Arg Glu Ile Arg Gln Arg Met Gly Glu Asp
283          100          105          110
286 Leu Glu Gly Leu Glu Ile Lys Glu Leu Arg Gly Leu Glu Gln Asn Met
287          115          120          125
290 Asp Glu Ala Leu Lys Leu Val Arg Asn Arg Lys Tyr His Val Ile Ser
291          130          135          140
294 Thr Gln Thr Asp Thr Phe Lys Lys Lys Leu Lys Asn Ser Gln Glu Thr
295 145          150          155          160
298 His Arg Asn Leu Leu Arg Glu Leu Glu Thr Glu His Ala Val Tyr Tyr
299          165          170          175
302 Val Asp Asp Asp Pro Asn Asn Tyr Asp Gly Ala Leu Ala Leu Gly Asn
303          180          185          190

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306 Gly Ala Ser Tyr Leu Tyr Ser Phe Arg Thr Gln Pro Ser Gln Pro Asn
307          195                      200                      205
310 Leu Gln Gly Val Gly Tyr Val Pro His Asp Leu Arg Leu Ala
311      210                      215                      220
314 <210> SEQ ID NO: 5
315 <211> LENGTH: 1036
316 <212> TYPE: DNA
317 <213> ORGANISM: Phalaenopsis equestris
320 <220> FEATURE:
321 <221> NAME/KEY: CDS
322 <222> LOCATION: (216)..(887)
324 <400> SEQUENCE: 5
325 acgcggggca ctggcttcac tttcttcctt ggggcaatgg ccaactattc ccggttaacta      60
327 tcgcttttgc gtttccagtt ctataaaagg aatccccgcc agagcttttt cttcttatag      120
329 agctttcttc ctcactcttc ccgttcgtca acatcactaa tcactgctgt ttcagtagac      180
331 tgggagagct aggagtggag aaaagagatt tgaag atg ggg agg ggg aag ata      233
332                               Met Gly Arg Gly Lys Ile
333                               1                      5
335 gag att aag aag ata gag aat ccg act aat cgg cag gtg acc tac tcg      281
336 Glu Ile Lys Lys Ile Glu Asn Pro Thr Asn Arg Gln Val Thr Tyr Ser
337          10                      15                      20
339 aag agg aga gct ggg att atg aag aag gcg agg gag atc act gtt ctc      329
340 Lys Arg Arg Ala Gly Ile Met Lys Lys Ala Arg Glu Ile Thr Val Leu
341          25                      30                      35
343 tgc gat gct gag gtt tcg ctt atc atg ttc tcg agt act ggg aag ttt      377
344 Cys Asp Ala Glu Val Ser Leu Ile Met Phe Ser Ser Thr Gly Lys Phe
345          40                      45                      50
347 tct gag tac tgt agc cct tcg acg gaa acg aag aag gtt ttt gaa cgc      425
348 Ser Glu Tyr Cys Ser Pro Ser Thr Glu Thr Lys Lys Val Phe Glu Arg
349 55                      60                      65                      70
351 tac cag cag gta tct ggc att aac ttg tgg agc tcg cag tac gag aag      473
352 Tyr Gln Gln Val Ser Gly Ile Asn Leu Trp Ser Ser Gln Tyr Glu Lys
353          75                      80                      85
355 atg ctg aat acg ctt aac cat tcg aag gag atc aat cgc aat ctg agg      521
356 Met Leu Asn Thr Leu Asn His Ser Lys Glu Ile Asn Arg Asn Leu Arg
357          90                      95                      100
359 agg gaa gta agg cag agg atg ggg gaa gat ctt gag gga ctg gat atc      569
360 Arg Glu Val Arg Gln Arg Met Gly Glu Asp Leu Glu Gly Leu Asp Ile
361          105                      110                      115
363 aag gaa ctg cgc ggt ctt gag caa aac att gat gag gca ttg aag cta      617
364 Lys Glu Leu Arg Gly Leu Glu Gln Asn Ile Asp Glu Ala Leu Lys Leu
365          120                      125                      130
367 gta cga aat aga aaa tat cat gta atc agt act caa acg gac acc tac      665
368 Val Arg Asn Arg Lys Tyr His Val Ile Ser Thr Gln Thr Asp Thr Tyr
369 135                      140                      145                      150
371 aag aag aag ttg aag aac tcc caa gaa aca cac cgg aac tta atg cac      713
372 Lys Lys Lys Leu Lys Asn Ser Gln Glu Thr His Arg Asn Leu Met His
373          155                      160                      165
375 gaa ttg gaa atc gtt gag gac cac cca gtg tat ggg ttc cac gag gat      761

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/08/2005
PATENT APPLICATION: US/10/690,246A TIME: 10:07:31

Input Set : A:\U0148638 sequence.txt
Output Set: N:\CRF4\08082005\J690246A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; Xaa Pos. 2

Seq#:26; Xaa Pos. 3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,48

VERIFICATION SUMMARY

DATE: 08/08/2005

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Input Set : A:\U0148638 sequence.txt

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L:808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0

L:828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0